SEQUENCE LISTING

<110>   Galloway, Susan May
        Davis, George Henry
        Gregan, Scott Michael
        Hanrahan, James Patrick
        Juengel, Jennifer Lee
        McNatty, Kenneth Pattrick
        Mulsant, Philippe
        Powell, Richard Patrick

<120>   NEW GDF-9 AND GDF-9B (BMP-15) SEQUENCES FOR
        ALTERING MAMMALIAN OVARIAN FUNCTION AND OVULATION RATE

<130>   AJPARK27.001APC

<140>   US 10/516992
<141>   2004-11-30

<150>   PCT/NZ03/00109
<151>   2003-05-30

<160>   18

<170>   PatentIn version 3.0

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phenylalanine

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c atg gcg ctt ccc  aac aaa ttc ttc ctt  tgg ttt tgc tgc ttt  gcc     166
  Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
      -315            -310                -305

tgg ctc tgt ttt  cct att agc ctt gat  tct ctg cct tct agg  gga         211
Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
        -300              -295              -290

gaa gct cag att  gta gct agg act gcg  ttg gaa tct gag gct  gag         256
Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
        -285              -280              -275

act tgg tcc ttg  ctg aac cat tta ggt  ggg aga cac aga cct  ggt         301
Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
        -270              -265              -260

ctc ctt tcc cct  ctc tta gag gtt ctg  tat gat ggg cac ggg  gaa         346
Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
        -255              -250              -245

ccc ccc agg ctg  cag cca gat gac aga  gct ttg cgc tac atg  aag         391
Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
        -240              -235              -230

agg ctc tat aag  gca tac gct acc aag  gag ggg acc cct aaa  tcc         436
Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
        -225              -220              -215

aac aga cgc cac  ctc tac aac act gtt  cgg ctc ttc acc ccc  tgt         481
Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
        -210              -205              -200

gct cag cac aag  cag gct cct ggg gac  ctg gcg gca g gtgtgtagga         528
Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala
        -195              -190

gcagattggt taatgggtgg agggaagaag aaagaccttt ttgcatttca gttacataaa    588

ggagttggcc ctgctccttg acttgcattt tactttgcat ggtactcaat atccaaacaa    648

acctggtgct tgatcttact tactgtttat tcctaatggc ctcatgggtt gatgtaggct    708

natcccaccc tgacgtttaa ggcttgagaa tgtggggaga aaagggacag aagcacattc    768

tgaggtactg attccttgat ttgacttcct gttacatatg cattactgt tggattgttt     828

ttcttctcag ga  acc  ttt cca tca gtg gat  ctg ctg ttt aac ctg  gat     876
           Gly Thr  Phe Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp

         -185                -180                -175
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cgt gtt act gtt  gtg gaa cat tta ttc  aag tca gtc ttg ctg  tat     921
Arg Val Thr Val  Val Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr
        -170              -165              -160

act ttc aac aac  tcc att tct ttt ccc  ttt cct gtt aaa tgt  ata     966
Thr Phe Asn Asn  Ser Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile
        -155              -150              -145

tgc aac ctg gtg  ata aaa gag cca gag  ttt tct agc aag act  ctc    1011
Cys Asn Leu Val  Ile Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu
        -140              -135              -130

cct aga gct cca  tac tca ttt acc tat  aac tca cag ttt gaa  ttt    1056
Pro Arg Ala Pro  Tyr Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe
        -125              -120              -115

aga aag aaa tac  aaa tgg atg gag att  gat gtg acg gct cct  ctt    1101
Arg Lys Lys Tyr  Lys Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu
        -110              -105              -100

gag cct ctg gtg  gcc tcc cac aag agg  aat att cac atg tct gta aat 1149
Glu Pro Leu Val  Ala Ser His Lys Arg  Asn Ile His Met Ser Val Asn
        -95               -90               -85

ttt aca tgt gcg  gaa gac cag ctg cag  cat cct tca gcg cgg gac agc 1197
Phe Thr Cys Ala  Glu Asp Gln Leu Gln  His Pro Ser Ala Arg Asp Ser
        -80               -75               -70

ctg ttt aac atg  act ctt ctc gta gcg  ccc tca ctg ctt ttg tat ctg 1245
Leu Phe Asn Met  Thr Leu Leu Val Ala  Pro Ser Leu Leu Leu Tyr Leu
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aac gac aca agt  gct cag gct ttt cac  agg tgg cat tcc ctc cac cct 1293
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aaa agg aag cct  tca cag ggt cct gac  cag aag aga ggg cta tct gcc 1341
Lys Arg Lys Pro  Ser Gln Gly Pro Asp  Gln Lys Arg Gly Leu Ser Ala
        -30               -25               -20

tac ccc gtg gga  gaa gaa gct gct gag  ggt gta aga tcg tcc cgt cac 1389
Tyr Pro Val Gly  Glu Glu Ala Ala Glu  Gly Val Arg Ser Ser Arg His
        -15               -10               -5

cgc aga gac cag  gag agt gcc agc tct  gaa ttg aag aag cct ctg gtt 1437
Arg Arg Asp Gln  Glu Ser Ala Ser Ser  Glu Leu Lys Lys Pro Leu Val
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cca gct tca gtc  aat ctg agt gaa tac  ttc aaa cag ttt ctt ttt ccc 1485
Pro Ala Ser Val  Asn Leu Ser Glu Tyr  Phe Lys Gln Phe Leu Phe Pro
15                20                25                30

cag aat gaa tgt  gag ctc cat gac ttt  aga ctt agc ttt agt cag ctg 1533
Gln Asn Glu Cys  Glu Leu His Asp Phe  Arg Leu Ser Phe Ser Gln Leu
        35                40                45

aag tgg gac aac  tgg att gtg gcc cca  cac aaa tac aac cct cga tac 1581
Lys Trp Asp Asn  Trp Ile Val Ala Pro  His Lys Tyr Asn Pro Arg Tyr
        50                55                60

tgt aaa ggg gac  tgt ccc agg gcg gtc  gga cat cgg tat ggc ttt ccg 1629
Cys Lys Gly Asp  Cys Pro Arg Ala Val  Gly His Arg Tyr Gly Phe Pro
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              65                    70                       75
gtt cac acc atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca     1677
Val His Thr Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser
    80                  85                  90

gtg cca aga cca tcc tgt gta cct gcc aag tat agc cct ttg agt gtt     1725
Val Pro Arg Pro Ser Cys Val Pro Ala Lys Tyr Ser Pro Leu Ser Val
95                  100                 105                 110

ttg gcc atc gag cct gat ggc tca atc gct tat aaa gaa tat gaa gat     1773
Leu Ala Ile Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp
                115                 120                 125

atg ata gcc act aag tgt acc tgt cgt taacagactc ctgtcaagta          1820
Met Ile Ala Thr Lys Cys Thr Cys Arg
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Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
          -300               -295               -290


Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
          -285               -280               -275


Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
          -270               -265               -260


Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
          -255               -250               -245


Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
          -240               -235               -230
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Arg Leu Tyr Lys Ala Tyr Ala Thr Lys Glu Gly Thr Pro Lys Ser
        -225   -220   -215

Asn Arg Arg His Leu Tyr Asn Thr Val Arg Leu Phe Thr Pro Cys
        -210   -205   -200

Ala Gln His Lys Gln Ala Pro Gly Asp Leu Ala Ala Gly Thr Phe
        -195   -190   -185

Pro Ser Val Asp Leu Leu Phe Asn Leu Asp Arg Val Thr Val Val
        -180   -175   -170

Glu His Leu Phe Lys Ser Val Leu Leu Tyr Thr Phe Asn Asn Ser
        -165   -160   -155

Ile Ser Phe Pro Phe Pro Val Lys Cys Ile Cys Asn Leu Val Ile
        -150   -145   -140

Lys Glu Pro Glu Phe Ser Ser Lys Thr Leu Pro Arg Ala Pro Tyr
        -135   -130   -125

Ser Phe Thr Tyr Asn Ser Gln Phe Glu Phe Arg Lys Lys Tyr Lys
        -120   -115   -110

Trp Met Glu Ile Asp Val Thr Ala Pro Leu Glu Pro Leu Val Ala Ser
        -105   -100   -95

His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
        -90   -85   -80

Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
    -75   -70   -65

Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
-60   -55   -50   -45

Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
            -40   -35   -30

Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
        -25   -20   -15

Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
    -10   -5   -1 1

Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu

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       5                   10                  15                  20
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Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
            25   30   35

His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
            40   45   50

Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
        55   60   65

Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
    70   75   80

Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
85   90   95   100

Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
            105   110   115

Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
            120   125   130

Thr Cys Arg
        135

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               -315                    -310                    -305
tgg ctc tgt ttt  cct att agc ctt gat  tct ctg cct tct agg  gga        90
Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
               -300                    -295                    -290

gaa gct cag att  gta gct agg act gcg  ttg gaa tct gag gct  gag       135
Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
               -285                    -280                    -275

act tgg tcc ttg  ctg aac cat tta ggt  ggg aga cac aga cct  ggt       180
Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
               -270                    -265                    -260

ctc ctt tcc cct  ctc tta gag gtt ctg  tat gat ggg cac ggg  gaa       225
Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
               -255                    -250                    -245

ccc ccc agg ctg  cag cca gat gac aga  gct ttg cgc tac atg  aag       270
Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
               -240                    -235                    -230

agg ctc tat aag  gca tac gct acc aag  gag ggg acc cct aaa  tcc       315
Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
               -225                    -220                    -215

aac aga cgc cac  ctc tac aac act gtt  cgg ctc ttc acc ccc  tgt       360
Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
               -210                    -205                    -200

gct cag cac aag  cag gct cct ggg gac  ctg gcg gca gga acc  ttt       405
Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe

               -195                    -190                    -185
cca tca gtg gat  ctg ctg ttt aac ctg  gat cgt gtt act gtt  gtg       450
Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp Arg Val Thr Val  Val
               -180                    -175                    -170

gaa cat tta ttc  aag tca gtc ttg ctg  tat act ttc aac aac  tcc       495
Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr Thr Phe Asn Asn  Ser
               -165                    -160                    -155

att tct ttt ccc  ttt cct gtt aaa tgt  ata tgc aac ctg gtg  ata       540
Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile Cys Asn Leu Val  Ile
               -150                    -145                    -140

aaa gag cca gag  ttt tct agc aag act  ctc cct aga gct cca  tac       585
Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu Pro Arg Ala Pro  Tyr
               -135                    -130                    -125

tca ttt acc tat  aac tca cag ttt gaa  ttt aga aag aaa tac  aaa       630
Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe Arg Lys Lys Tyr  Lys
               -120                    -115                    -110

tgg atg gag att  gat gtg acg gct cct  ctt gag cct ctg gtg gcc tcc   678
Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu Glu Pro Leu Val Ala Ser
               -105                    -100                    -95

cac aag agg aat att cac atg tct gta aat ttt aca tgt gcg gaa gac     726
His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
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cag ctg cag cat cct tca gcg cgg gac agc ctg ttt aac atg act ctt          774
Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
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ctc gta gcg ccc tca ctg ctt ttg tat ctg aac gac aca agt gct cag          822
Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
-60             -55             -50                         -45

gct ttt cac agg tgg cat tcc ctc cac cct aaa agg aag cct tca cag          870
Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
                -40             -35                 -30

ggt cct gac cag aag aga ggg cta tct gcc tac ccc gtg gga gaa gaa          918
Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
            -25             -20             -15

gct gct gag ggt gta aga tcg tcc cgt cac cgc aga gac cag gag agt          966
Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
        -10             -5              -1  1

gcc agc tct gaa ttg aag aag cct ctg gtt cca gct tca gtc aat ctg         1014
Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
5               10              15              20

agt gaa tac ttc aaa cag ttt ctt ttt ccc cag aat gaa tgt gag ctc         1062
Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
            25              30              35

cat gac ttt aga ctt agc ttt agt cag ctg aag tgg gac aac tgg att         1110
His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
            40              45              50

gtg gcc cca cac aaa tac aac cct cga tac tgt aaa ggg gac tgt ccc         1158
Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
        55              60              65

agg gcg gtc gga cat cgg tat ggc ttt ccg gtt cac acc atg gtg cag         1206
Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
    70              75              80

aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga cca tcc tgt         1254
Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
85              90              95              100

gta cct gcc aag tat agc cct ttg agt gtt ttg gcc atc gag cct gat         1302
Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
            105             110             115

ggc tca atc gct tat aaa gaa tat gaa gat atg ata gcc act aag tgt         1350
Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
            120             125             130

acc tgt cgt taa                                                         1362
Thr Cys Arg
        135


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<212>   PRT
<213>   Ovis aries
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Trp Leu Cys Phe Pro Ile Ser Leu Asp Ser Leu Pro Ser Arg Gly
            -300   -295   -290

Glu Ala Gln Ile Val Ala Arg Thr Ala Leu Glu Ser Glu Ala Glu
            -285   -280   -275

Thr Trp Ser Leu Leu Asn His Leu Gly Gly Arg His Arg Pro Gly
            -270   -265   -260

Leu Leu Ser Pro Leu Leu Glu Val Leu Tyr Asp Gly His Gly Glu
            -255   -250   -245

Pro Pro Arg Leu Gln Pro Asp Asp Arg Ala Leu Arg Tyr Met Lys
            -240   -235   -230

Arg Leu Tyr Lys Ala Tyr Ala Thr Lys Glu Gly Thr Pro Lys Ser
            -225   -220   -215

Asn Arg Arg His Leu Tyr Asn Thr Val Arg Leu Phe Thr Pro Cys
            -210   -205   -200

Ala Gln His Lys Gln Ala Pro Gly Asp Leu Ala Ala Gly Thr Phe
            -195   -190   -185

Pro Ser Val Asp Leu Leu Phe Asn Leu Asp Arg Val Thr Val Val
            -180   -175   -170

Glu His Leu Phe Lys Ser Val Leu Leu Tyr Thr Phe Asn Asn Ser
            -165   -160   -155

Ile Ser Phe Pro Phe Pro Val Lys Cys Ile Cys Asn Leu Val Ile
            -150   -145   -140

Lys Glu Pro Glu Phe Ser Ser Lys Thr Leu Pro Arg Ala Pro Tyr
            -135   -130   -125

Ser Phe Thr Tyr Asn Ser Gln Phe Glu Phe Arg Lys Lys Tyr Lys

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                -120                     -115                    -110
Trp Met Glu Ile Asp Val Thr Ala Pro  Leu Glu Pro Leu Val Ala Ser
                -105                    -100                    -95

His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
            -90             -85             -80

Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
    -75             -70             -65

Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
-60             -55             -50                         -45

Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
            -40             -35             -30

Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
            -25             -20             -15

Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
        -10             -5              -1  1

Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
5               10              15                          20

Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
            25              30              35

His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
            40              45              50

Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
        55              60              65

Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
    70              75              80

Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
85              90              95                          100

Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
            105             110             115

Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
            120             125             130
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Thr Cys Arg
           135

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phenylalanine

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aac tgg att gtg gcc cca cac aaa tac aac cct cga tac tgt aaa ggg   48
Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly
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gac tgt ccc agg gcg gtc gga cat cgg tat ggc ttt ccg gtt cac acc   96
Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr
            20   25   30

atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga   144
Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg
        35   40   45

cca tcc tgt gta cct gcc aag tat   168
Pro Ser Cys Val Pro Ala Lys Tyr
    50   55

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<213> Ovis aries

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Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly
1   5   10   15

Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr
            20   25   30

Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg
        35   40   45

Pro Ser Cys Val Pro Ala Lys Tyr
    50   55

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<223>  n at 685 represents remainder of approx 5.2 kb intron.
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<221>  misc_feature
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<223>  position of first codon of mature peptide in wildtype sheep.
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<221>  misc_feature
<222>  (1628)..(1630)
<223>  tga stop codon in wildtype sheep.
<220>
<221>  3'UTR
<222>  (1631)..(1665)
<220>
<221>  mutation
<222>  (1166)..(1168)
<223>  c to t at 1166 of [S1] sheep changes cag glutamine codon to tag STOP
```

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<400>  7
catgctgcct tgtcccacct gctgtttctg tttgtttgat gcaaagagga caatttagaa      60

gacctctttt tggttcagga gatcctacca gaggaagaaa cataggacct gcctgccagc     120

ctttcatttt tccttgccct atcctttgtg gtagtggagc ctggatgctg ttacccatgt     180

aaaaggaaag gtttaaagcg ttatcctttg ggcttttatc agaacatgtt gctgaacacc     240

aagcttttca ag atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga     291
              Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly
               1               5                  10

ctg gtg ctt ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag      339
Leu Val Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln
    15              20                  25

ccc tct att gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag      387
Pro Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
30              35                  40                  45

gag ctg cta gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc      435
Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val
                50                  55                  60

tta ggg cat ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct      483
Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala
                65                  70                  75
```

```
gac gca agt gga cac cct agg gaa aac cgc acc att ggg gcc acc atg       531
Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met
        80                  85                  90

gtg agg ctg gtg agg ccg ctg gct agt gta gca agg cct ctc aga g         577


Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg
    95                  100                 105

gtgagttatc atactatatt gttctggtgg gagggggga gaaaatgggg aagaaaagtg      637

tagaaaaaag tggatctgtc agttttctgt caggcttcac attgcctnca gtttgtactg      697

agcaggtctg ttagagagac taaggctagg atataagaag ctaacgcttt gctcttgttc      757

cctcttacta atgcag gc  tcc tgg cac ata cag acc ctg gac ttt cct ctg      808
                Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu
                    110                 115                 120

aga cca aac cgg gta gca tac caa cta gtc aga gcc act gtg gtt tac       856
Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val Tyr
                125                 130                 135

cgc cat cag ctt cac cta act cat tcc cac ctc tcc tgc cat gtg gag       904
Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His Val Glu
            140                 145                 150

ccc tgg gtc cag aaa agc cca acc aat cac ttt cct tct tca gga aga       952
Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser Ser Gly Arg
        155                 160                 165

ggc tcc tca aag cct tcc ctg ttg ccc aaa act tgg aca gag atg gat       1000
Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp
    170                 175                 180

atc atg gaa cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg       1048
Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Arg
185                 190                 195                 200

gtt cta cga ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt       1096
Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val
                205                 210                 215

ctt gag ttc tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg       1144
Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu
                220                 225                 230

tta ctg tat ttc aat gac act tagagtgttc agaagaccaa acctctccct          1195
Leu Leu Tyr Phe Asn Asp Thr
    235

aaaggcctga aagagtttac agaaaaagac ccttctcttc tcttgaggag ggctcgtcaa      1255

gcaggcagta ttgcatcgga agttcctggc ccctccaggg agcatgatgg gcctgaaagt      1315

aaccagtgtt ccctccaccc ttttcaagtc agcttccagc agctgggctg ggatcactgg      1375

atcattgctc cccatctcta taccccaaac tactgtaagg gagtatgtcc tcgggtacta      1435

cactatggtc tcaattctcc caatcatgcc atcatccaga accttgtcag tgagctggtg      1495
```

gatcagaatg tccctcagcc ttcctgtgtc ccttataagt atgttcccat tagcatcctt   1555

ctgattgagg caaatgggag tatcttgtac aaggagtatg agggtatgat tgcccagtcc   1615

tgcacatgca ggtgacggca aaggtgcagc tagctcaggt ttcccaagaa   1665

<210> 8
<211> 239
<212> PRT
<213> Ovis aries
<220>
<221> misc_feature
<222> (253)..(255)
<223> atg start codon.
<220>
<221> misc_feature
<222> (1253)..(1255)
<223> position of first codon of mature peptide in wildtype sheep.
<220>
<221> misc_feature
<222> (685)..()
<223> n represents approx 5.2 kb of intron.
<220>
<221> misc_feature
<222> (1628)..(1630)
<223> tga stop codon in wildtype sheep.

<400> 8

Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
1   5   10   15

Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
            20   25   30

Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
        35   40   45

Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
    50   55   60

Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65   70   75   80

Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
            85   90   95

Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
            100   105   110

Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
        115   120   125

Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His

```
            130                   135                   140
```

```
Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
145                 150                 155                 160


Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
                165                 170                 175


Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
            180                 185                 190


Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
        195                 200                 205


Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
    210                 215                 220


Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
225                 230                 235
```

```
<210>  9
<211>  1182
<212>  DNA
<213>  Ovis areis
<220>
<221>  misc_feature
<222>  (1)..(3)
<223>  atg start codon
<220>
<221>  mutation
<222>  (718)..(720)
<223>  c to t at 718 of [S1] sheep changes cag glutamine codon to tag STOP.
<220>
<221>  CDS
<222>  (1)..(717)
<220>
<221>  misc_feature
<222>  (805)..(807)
<223>  first codon of mature peptide in wildtype sheep.
<220>
<221>  misc_feature
<222>  (1180)..(1182)
<223>  tga stop codon.

<400>  9
atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga ctg gtg ctt      48
Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
1               5                   10                  15


ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag ccc tct att      96
Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
                20                  25                  30


gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag gag ctg cta     144
Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
```

```
gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc tta ggg cat      192
Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
        50                  55                  60


ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct gac gca agt      240
Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65                  70                  75                  80


gga cac cct agg gaa aac cgc acc att ggg gcc acc atg gtg agg ctg      288
Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
                85                  90                  95


gtg agg ccg ctg gct agt gta gca agg cct ctc aga ggc tcc tgg cac      336
Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
            100                 105                 110


ata cag acc ctg gac ttt cct ctg aga cca aac cgg gta gca tac caa      384
Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
            115                 120                 125


cta gtc aga gcc act gtg gtt tac cgc cat cag ctt cac cta act cat      432
Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
        130                 135                 140


tcc cac ctc tcc tgc cat gtg gag ccc tgg gtc cag aaa agc cca acc      480
Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
145                 150                 155                 160


aat cac ttt cct tct tca gga aga ggc tcc tca aag cct tcc ctg ttg      528
Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
                165                 170                 175


ccc aaa act tgg aca gag atg gat atc atg gaa cat gtt ggg caa aag      576
Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
            180                 185                 190


ctc tgg aat cac aag ggg cgc agg gtt cta cga ctc cgc ttc gtg tgt      624
Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
        195                 200                 205


cag cag cca aga ggt agt gag gtt ctt gag ttc tgg tgg cat ggc act      672


Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
    210                 215                 220


tca tca ttg gac act gtc ttc ttg tta ctg tat ttc aat gac act          717
Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
225                 230                 235


tagagtgttc agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac    777

ccttctcttc tcttgaggag ggctcgtcaa gcaggcagta ttgcatcgga agttcctggc    837

ccctccaggg agcatgatgg gcctgaaagt aaccagtgtt ccctccaccc ttttcaagtc    897

agcttccagc agctgggctg ggatcactgg atcattgctc cccatctcta taccccaaac    957

tactgtaagg gagtatgtcc tcgggtacta cactatggtc tcaattctcc caatcatgcc    1017

atcatccaga accttgtcag tgagctggtg gatcagaatg tccctcagcc ttcctgtgtc    1077
```

ccttataagt atgttcccat tagcatcctt ctgattgagg caaatgggag tatcttgtac   1137

aaggagtatg agggtatgat tgcccagtcc tgcacatgca ggtga   1182

<210>   10
<211>   239
<212>   PRT
<213>   Ovis areis
<220>
<221>   misc_feature
<222>   (1)..(3)
<223>   atg start codon.
<220>
<221>   misc_feature
<222>   (805)..(807)
<223>   first codon of mature peptide in wildtype sheep.
<220>
<221>   misc_feature
<222>   (1180)..(1182)
<223>   tga stop codon.

<400>   10

Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
1   5   10   15

Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
            20   25   30

Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
        35   40   45

Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His

    50   55   60

Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65   70   75   80

Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
            85   90   95

Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
            100   105   110

Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
            115   120   125

Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
        130   135   140

Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr

145   150   155   160

Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
            165   170   175

Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
            180   185   190

Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
            195   200   205

Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
   210   215   220

Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
225   230   235

```
<210>  11
<211>  168
<212>  DNA
<213>  Ovis aries
<220>
<221>  CDS
<222>  (1)..(84)
<220>
<221>  mutation
<222>  (85)..(87)
<223>  c to t at 85 of [S1] sheep changes glutamine cag codon to tag STOP

<400>  11
aga ggt agt gag gtt ctt gag ttc tgg tgg cat ggc act tca tca ttg        48
Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu
1               5                   10                  15

gac act gtc ttc ttg tta ctg tat ttc aat gac act tagagtgttc           94
Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
                20                  25

agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac ccttctcttc     154

tcttgaggag ggct                                                      168


<210>  12
<211>  28
<212>  PRT
<213>  Ovis aries

<400>  12

Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu
1               5                   10                  15

Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
                20                  25
```

```
<210> 13
<211> 1665
<212> DNA
<213> Ovis aries
<220>
<221> 5'UTR
<222> (1)..(252)
<220>
<221> misc_feature
<222> (253)..(255)
<223> atg start codon.
<220>
<221> CDS
<222> (253)..(577)
<220>
<221> CDS
<222> (774)..(1627)
<220>
<221> Intron
<222> (578)..(773)
<223> n at 685 represents approx 5.2 kb intron.
<220>
<221> mat_peptide
<222> (1253)..()
<220>
<221> misc_feature
<222> (685)..()
<223> n represents approx 5.2 kb of intron
<220>
<221> misc_feature
<222> (1628)..(1630)
<223> tga stop codon.
<220>
<221> 3'UTR
<222> (1628)..(1665)
<220>
<221> mutation
<222> (1547)..(1549)
<223> g to t at 1548 of [S2] sheep changes agc serine codon to atc
isoleucine codon

<400> 13
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catgctgcct  tgtcccacct  gctgtttctg  tttgtttgat  gcaaagagga  caatttagaa     60

gacctctttt  tggttcagga  gatcctacca  gaggaagaaa  cataggacct  gcctgccagc    120

ctttcatttt  tccttgccct  atcctttgtg  gtagtggagc  ctggatgctg  ttacccatgt    180

aaaaggaaag  gtttaaagcg  ttatcctttg  ggcttttatc  agaacatgtt  gctgaacacc    240

aagcttttca  ag atg gtc ctc ctg  agc atc ctt aga atc  ctt ctt tgg           288
              Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp
                      -265                  -260

gga ctg  gtg ctt ttt atg gaa  cat agg gtc caa atg  aca cag gta             333
Gly Leu  Val Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val
    -255              -250                  -245

ggg cag  ccc tct att gcc cac  ctg cct gag gcc cct  acc ttg ccc             378
Gly Gln  Pro Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro
    -240              -235                  -230
```

```
ctg att  cag gag ctg cta gaa  gaa gcc cct ggc aag  cag cag agg      423
Leu Ile  Gln Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg
    -225              -220              -215

aag ccg  cgg gtc tta ggg cat  ccc tta cgg tat atg  ctg gag ctg      468
Lys Pro  Arg Val Leu Gly His  Pro Leu Arg Tyr Met  Leu Glu Leu
    -210              -205              -200

tac cag  cgt tca gct gac gca  agt gga cac cct agg  gaa aac cgc      513
Tyr Gln  Arg Ser Ala Asp Ala  Ser Gly His Pro Arg  Glu Asn Arg
    -195              -190              -185

acc att  ggg gcc acc atg gtg  agg ctg gtg agg ccg  ctg gct agt      558
Thr Ile  Gly Ala Thr Met Val  Arg Leu Val Arg Pro  Leu Ala Ser
    -180              -175              -170

gta gca  agg cct ctc aga g gtgagttatc atactatatt gttctggtgg        607
Val Ala  Arg Pro Leu Arg
    -165

gaggggggga gaaaatgggg aagaaaagtg tagaaaaaag tggatctgtc agttttctgt   667

caggcttcac attgcctnca gtttgtactg agcaggtctg ttagagagac taaggctagg   727

atataagaag ctaacgcttt gctcttgttc cctcttacta atgcag gc   tcc tgg     781
                                                   Gly  Ser Trp
                                                   -160

cac ata cag  acc ctg gac ttt cct  ctg aga cca aac cgg  gta gca      826


His Ile Gln  Thr Leu Asp Phe Pro  Leu Arg Pro Asn Arg  Val Ala
        -155              -150              -145

tac caa cta  gtc aga gcc act gtg  gtt tac cgc cat cag  ctt cac      871
Tyr Gln Leu  Val Arg Ala Thr Val  Val Tyr Arg His Gln  Leu His
        -140              -135              -130

cta act cat  tcc cac ctc tcc tgc  cat gtg gag ccc tgg  gtc cag      916
Leu Thr His  Ser His Leu Ser Cys  His Val Glu Pro Trp  Val Gln
        -125              -120              -115

aaa agc cca  acc aat cac ttt cct  tct tca gga aga ggc  tcc tca      961
Lys Ser Pro  Thr Asn His Phe Pro  Ser Ser Gly Arg Gly  Ser Ser
        -110              -105              -100

aag cct tcc ctg ttg ccc aaa act tgg aca gag atg gat atc atg gaa    1009
Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu
        -95              -90              -85

cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg gtt cta cga    1057
His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg
        -80              -75              -70

ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt ctt gag ttc    1105
Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe
-65              -60              -55              -50

tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg tta ctg tat    1153
Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr
            -45              -40              -35

ttc aat gac act cag agt gtt cag aag acc aaa cct ctc cct aaa ggc    1201
```

```
Phe Asn Asp Thr Gln Ser Val Gln Lys Thr Lys Pro Leu Pro Lys Gly
        -30               -25               -20


ctg aaa gag ttt aca gaa aaa gac cct tct ctt ctc ttg agg agg gct      1249
Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser Leu Leu Leu Arg Arg Ala
        -15               -10               -5


cgt caa gca ggc agt att gca tcg gaa gtt cct ggc ccc tcc agg gag      1297
Arg Gln Ala Gly Ser Ile Ala Ser Glu Val Pro Gly Pro Ser Arg Glu
-1  1             5                 10                15


cat gat ggg cct gaa agt aac cag tgt tcc ctc cac cct ttt caa gtc      1345
His Asp Gly Pro Glu Ser Asn Gln Cys Ser Leu His Pro Phe Gln Val
             20                25                30


agc ttc cag cag ctg ggc tgg gat cac tgg atc att gct ccc cat ctc      1393
Ser Phe Gln Gln Leu Gly Trp Asp His Trp Ile Ile Ala Pro His Leu
             35                40                45


tat acc cca aac tac tgt aag gga gta tgt cct cgg gta cta cac tat      1441
Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys Pro Arg Val Leu His Tyr
         50                55                60


ggt ctc aat tct ccc aat cat gcc atc atc cag aac ctt gtc agt gag      1489
Gly Leu Asn Ser Pro Asn His Ala Ile Ile Gln Asn Leu Val Ser Glu
         65                70                75


ctg gtg gat cag aat gtc cct cag cct tcc tgt gtc cct tat aag tat      1537
Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr Lys Tyr
80                85                90                95


gtt ccc att atc atc ctt ctg att gag gca aat ggg agt atc ttg tac      1585
Val Pro Ile Ile Ile Leu Leu Ile Glu Ala Asn Gly Ser Ile Leu Tyr
             100               105               110


aag gag tat gag ggt atg att gcc cag tcc tgc aca tgc agg              1627
Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser Cys Thr Cys Arg
             115               120               125


tgacggcaaa ggtgcagcta gctcaggttt cccaagaa                           1665
```

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<210>  14
<211>  393
<212>  PRT
<213>  Ovis aries
<220>
<221>  misc_feature
<222>  (253)..(255)
<223>  atg start codon.
<220>
<221>  misc_feature
<222>  (685)..()
<223>  n represents approx 5.2 kb of intron
<220>
<221>  misc_feature
<222>  (1628)..(1630)
<223>  tga stop codon.

<400>  14
```

```
Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val
        -265              -260              -255
```

Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro
            -250   -245   -240

Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
            -235   -230   -225

Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg
            -220   -215   -210

Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg
            -205   -200   -195

Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly
            -190   -185   -180

Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg
            -175   -170   -165

Pro Leu Arg Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu
            -160   -155   -150

Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val
            -145   -140   -135

Tyr Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His
            -130   -125   -120

Val Glu Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser
            -115   -110   -105

Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr
            -100   -95   -90

Glu Met Asp Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys
        -85   -80   -75

Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly
    -70   -65   -60

Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr
-55   -50   -45   -40

Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr
            -35   -30   -25

Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser

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```
        -20                    -15                    -10

Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
         -5              -1  1                 5

Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser
10              15                 20                     25

Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp
             30              35                     40

Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
             45              50                     55

Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
        60              65                 70

Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser

    75                  80                     85

Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
90              95                 100                    105

Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
             110             115                    120

Cys Thr Cys Arg
             125
```

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<210>  15
<211>  1182
<212>  DNA
<213>  Ovis aries
<220>
<221>  misc_feature
<222>  (1)..(3)
<223>  atg start codon.
<220>
<221>  mutation
<222>  (1099)..(1101)
<223>  g to to at 1100 of [S2] sheep changes agc serine codon to atc
isoleucine codon
<220>
<221>  CDS
<222>  (1)..(1179)
<220>
<221>  mat_peptide
<222>  (805)..()
<220>
<221>  misc_feature
<222>  (1180)..(1182)
<223>  tga stop codon.
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<400> 15

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atg gtc ctc ctg  agc atc ctt aga atc  ctt ctt tgg gga ctg  gtg       45
Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp Gly Leu  Val
        -265              -260                  -255

ctt ttt atg gaa  cat agg gtc caa atg  aca cag gta ggg cag  ccc       90
Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val Gly Gln  Pro
        -250              -245                  -240

tct att gcc cac  ctg cct gag gcc cct  acc ttg ccc ctg att  cag      135
Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro Leu Ile  Gln
        -235              -230                  -225

gag ctg cta gaa  gaa gcc cct ggc aag  cag cag agg aag ccg  cgg      180
Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg Lys Pro  Arg
        -220              -215                  -210

gtc tta ggg cat  ccc tta cgg tat atg  ctg gag ctg tac cag  cgt      225
Val Leu Gly His  Pro Leu Arg Tyr Met  Leu Glu Leu Tyr Gln  Arg
        -205              -200                  -195

tca gct gac gca  agt gga cac cct agg  gaa aac cgc acc att  ggg      270
Ser Ala Asp Ala  Ser Gly His Pro Arg  Glu Asn Arg Thr Ile  Gly
        -190              -185                  -180

gcc acc atg gtg  agg ctg gtg agg ccg  ctg gct agt gta gca  agg      315
Ala Thr Met Val  Arg Leu Val Arg Pro  Leu Ala Ser Val Ala  Arg
        -175              -170                  -165

cct ctc aga ggc  tcc tgg cac ata cag  acc ctg gac ttt cct  ctg      360
Pro Leu Arg Gly  Ser Trp His Ile Gln  Thr Leu Asp Phe Pro  Leu
        -160              -155                  -150

aga cca aac cgg  gta gca tac caa cta  gtc aga gcc act gtg  gtt      405
Arg Pro Asn Arg  Val Ala Tyr Gln Leu  Val Arg Ala Thr Val  Val
        -145              -140                  -135

tac cgc cat cag  ctt cac cta act cat  tcc cac ctc tcc tgc  cat      450
Tyr Arg His Gln  Leu His Leu Thr His  Ser His Leu Ser Cys  His
        -130              -125                  -120

gtg gag ccc tgg  gtc cag aaa agc cca  acc aat cac ttt cct  tct      495
Val Glu Pro Trp  Val Gln Lys Ser Pro  Thr Asn His Phe Pro  Ser
        -115              -110                  -105

tca gga aga ggc  tcc tca aag cct tcc  ctg ttg ccc aaa act tgg aca   543
Ser Gly Arg Gly  Ser Ser Lys Pro Ser  Leu Leu Pro Lys Thr Trp Thr
        -100              -95                   -90

gag atg gat atc  atg gaa cat gtt ggg  caa aag ctc tgg aat cac aag   591
Glu Met Asp Ile  Met Glu His Val Gly  Gln Lys Leu Trp Asn His Lys
        -85               -80                   -75

ggg cgc agg gtt  cta cga ctc cgc ttc  gtg tgt cag cag cca aga ggt   639
Gly Arg Arg Val  Leu Arg Leu Arg Phe  Val Cys Gln Gln Pro Arg Gly
    -70               -65                   -60

agt gag gtt ctt  gag ttc tgg tgg cat  ggc act tca tca ttg gac act   687
Ser Glu Val Leu  Glu Phe Trp Trp His  Gly Thr Ser Ser Leu Asp Thr
-55               -50                   -45                    -40
```

```
gtc ttc ttg tta ctg tat ttc aat gac act cag agt gtt cag aag acc        735
Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr
            -35               -30                   -25

aaa cct ctc cct aaa ggc ctg aaa gag ttt aca gaa aaa gac cct tct        783
Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser
            -20               -15                   -10

ctt ctc ttg agg agg gct cgt caa gca ggc agt att gca tcg gaa gtt        831
Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
            -5               -1  1                  5

cct ggc ccc tcc agg gag cat gat ggg cct gaa agt aac cag tgt tcc        879
Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser
10                   15                   20                   25

ctc cac cct ttt caa gtc agc ttc cag cag ctg ggc tgg gat cac tgg        927
Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp
            30               35                   40

atc att gct ccc cat ctc tat acc cca aac tac tgt aag gga gta tgt        975
Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
            45               50                   55

cct cgg gta cta cac tat ggt ctc aat tct ccc aat cat gcc atc atc       1023
Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
            60               65                   70

cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct cag cct tcc       1071
Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
    75                   80                   85

tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg att gag gca       1119
Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
90                   95                   100                  105

aat ggg agt atc ttg tac aag gag tat gag ggt atg att gcc cag tcc       1167
Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
            110                  115                  120

tgc aca tgc agg tga                                                    1182
Cys Thr Cys Arg
            125
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<210>   16
<211>   393
<212>   PRT
<213>   Ovis aries
<220>
<221>   misc_feature
<222>   (1)..(3)
<223>   atg start codon.
<220>
<221>   misc_feature
<222>   (1180)..(1182)
<223>   tga stop codon.

<400>   16
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Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp Gly Leu  Val
            -265                -260                   -255
```

Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro
          -250   -245   -240

Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
          -235   -230   -225

Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg
          -220   -215   -210

Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg
          -205   -200   -195

Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly
          -190   -185   -180

Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg
          -175   -170   -165

Pro Leu Arg Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu
          -160   -155   -150

Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val
          -145   -140   -135

Tyr Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His
          -130   -125   -120

Val Glu Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser
          -115   -110   -105

Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr
          -100   -95   -90

Glu Met Asp Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys
          -85   -80   -75

Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly
          -70   -65   -60

Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr
-55   -50   -45   -40

Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr
               -35   -30   -25

Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser
          -20   -15   -10

```
Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
        -5              -1  1               5


Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser
10              15              20                      25


Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp
                30              35                      40


Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
            45              50              55


Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
        60              65              70


Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
    75              80              85


Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
90              95              100                     105


Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
            110             115             120


Cys Thr Cys Arg
            125


<210>   17
<211>   168
<212>   DNA
<213>   Ovis aries
<220>
<221>   CDS
<222>   (1)..(168)
<220>
<221>   mutation
<222>   (85)..(87)
<223>   g to t at 86 of GDF9B sheep changes agc serine codon to atc
isoleucine codon

<400>   17
gcc atc atc cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct        48
Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro
1               5               10                      15


cag cct tcc tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg        96
Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu
                20              25              30


att gag gca aat ggg agt atc ttg tac aag gag tat gag ggt atg att       144
Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile
```

```
           35                   40                   45                      168
gcc cag tcc tgc aca tgc agg tga
Ala Gln Ser Cys Thr Cys Arg
   50                   55


<210>  18
<211>  55
<212>  PRT
<213>  Ovis aries

<400>  18

Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro
1                   5                  10                  15


Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu
               20                  25                  30


Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile
           35                  40                  45


Ala Gln Ser Cys Thr Cys Arg
           50                  55
```